

Day 7 Worksheet – Installing Rsubread

Author: Rutendo Sigauke

This short worksheet goes over installing Rsubread in R on the AWS. This process can take a while and should be completed before class. RSubread can be found on Bioconductor and instructions to install the package can be found here:

<https://bioconductor.org/packages/release/bioc/html/Rsubread.html>.

Install Rsubread:

Installation can be done in the R console (shown below).

- Type **R** in the terminal

```
[rutendos@ip-172-31-18-92 ~]$ R

R version 3.6.0 (2019-04-26) -- "Planting of a Tree"
Copyright (C) 2019 The R Foundation for Statistical Computing
Platform: x86_64-redhat-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

- Rsubread can be found on the **BiocManager**, so to install the counting library, we have to first install **BiocManager**. **BiocManager** library can be installed from the R Comprehensive R Archive Network (CRAN).

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
```

```
> if (!requireNamespace("BiocManager", quietly = TRUE)) ## Install BiocManager
[+ install.packages("BiocManager")
Installing package into '/usr/lib64/R/library'
(as 'lib' is unspecified)
Warning in install.packages("BiocManager") :
  'lib = "/usr/lib64/R/library"' is not writable
Would you like to use a personal library instead? (yes/No/cancel) yes
Would you like to create a personal library
'~/R/x86_64-redhat-linux-gnu-library/3.6'
to install packages into? (yes/No/cancel) yes
```

- The above command will initiate a new personal library for your R packages. Select **yes**. Additionally, CRAN mirrors from where to download the packages. We will use the USA (KS) mirror.

```
--- Please select a CRAN mirror for use in this session ---
Secure CRAN mirrors
```

```
1: 0-Cloud [https]
2: Australia (Canberra) [https]
3: Australia (Melbourne 1) [https]
4: Australia (Melbourne 2) [https]
5: Australia (Perth) [https]
6: Austria [https]
7: Belgium (Brussels) [https]
8: Brazil (PR) [https]
9: Brazil (RJ) [https]
10: Brazil (SP 1) [https]
11: Brazil (SP 2) [https]
```

```
71: USA (IA) [https]
72: USA (KS) [https]
73: USA (MI) [https]
74: USA (OH) [https]
75: USA (OR) [https]
76: USA (TN) [https]
77: USA (TX 1) [https]
78: Uruguay [https]
79: (other mirrors)
```

```
Selection: 72
```

- Now, we can install **Rsubread** from **BiocManager** to our **R** libraries.

```
BiocManager::install("Rsubread")
```

```

[> BiocManager::install("Rsubread")
'getOption("repos")' replaces Bioconductor standard repositories, see
'?repositories' for details

replacement repositories:
  CRAN: https://rweb.crmda.ku.edu/cran

Bioconductor version 3.10 (BiocManager 1.30.18), R 3.6.0 (2019-04-26)
Installing package(s) 'BiocVersion', 'Rsubread'
trying URL 'https://bioconductor.org/packages/3.10/bioc/src/contrib/BiocVersion_3.10.1.tar.gz'
Content type 'application/x-gzip' length 984 bytes
=====
downloaded 984 bytes

```

NB: This will take a few seconds. If the library is installed successfully, it can be loaded as shown below without any errors.

```

[> library("Rsubread")

```

If the above does not work, try installing from source:

In some cases, you may have to download an older version of Rsubread from source (<https://bioconductor.org/packages/3.17/bioc/src/contrib/Archive/Rsubread/>).

- First, download the tar.gz file with wget to a location on the AWS.

wget

```

https://bioconductor.org/packages/3.17/bioc/src/contrib/Archive/Rsubread/Rsub
read_2.14.0.tar.gz

```

- Open R and install the package from the source file as shown below.

```

install.packages("/path_to_file/Rsubread_2.14.0.tar.gz", repos = NULL,
type="source")

```